

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/006,366

DATE: 12/17/2001
TIME: 11:09:46

Input Set : A:\RTS-0332 Sequence Listing.txt
Output Set: N:\CRF3\12172001\J006366.raw

ENTERED

6 <110> APPLICANT: C. Frank Bennett
7 Kenneth W. Dobie
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MHC CLASS II TRANSACTIVATOR

EXPRESSION

11 <130> FILE REFERENCE: RTS-0332
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/006,366
C--> 13 <141> CURRENT FILING DATE: 2001-11-05
13 <160> NUMBER OF SEQ ID NOS: 98
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
26 tccgtcatcg ctctcaggg 20
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
39 atgcattctg cccccaagga 20
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 6672
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (139)...(3531)
52 <400> SEQUENCE: 3
53 cctcccaact ggtgactggg tagtgatgag gctgtgtgct tctgagctgg gcatccgaag 60
54 gcatccttgg ggaagctgag ggcacgagga ggggctgcca gactccggga gctgtgctc 120
55 gggctgggatt cctacaca atg cgt tgc ctg gct cca cgc cct gct ggg tcc 171
56 Met Arg Cys Leu Ala Pro Arg Pro Ala Gly Ser
57 1 5 10
59 tac ctg tca gag ccc caa ggc agc tca cag tgt gcc acc atg gag ttg 219
60 Tyr Leu Ser Glu Pro Gln Gly Ser Ser Gln Cys Ala Thr Met Glu Leu
61 15 20 25
63 ggg ccc cta gaa ggt ggc tac ctg gag ctt ctt aac agc gat gct gac 267
64 Gly Pro Leu Glu Gly Tyr Leu Leu Leu Asn Ser Asp Ala Asp
65 30 35 40
67 ccc ctg tgc etc tac cac ttc tat gac cag atg gac ctg gct gga gaa 315
68 Pro Leu Cys Leu Tyr His Phe Tyr Asp Gln Met Asp Leu Ala Gly Glu
69 45 50 55
71 gaa gag att gag ctg tac tca gaa ccc gac aca gac acc atc aac tgc 363
72 Glu Glu Ile Glu Leu Tyr Ser Glu Pro Asp Thr Asp Thr Ile Asn Cys

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73	60		65		70		75	411
75	gac	cag	ttc	agc	agg	ctg	ttg	tgt
76	Asp	Gln	Phe	Ser	Arg	Leu	Leu	Cys
77								
79	agg	gag	gct	tat	gcc	aat	atc	gcg
80	Arg	Glu	Ala	Tyr	Ala	Asn	Ile	Ala
81								
83	gac	tcc	cag	ctg	gag	ggc	ctg	agc
84	Asp	Ser	Gln	Leu	Glu	Gly	Leu	Ser
85								
87	cca	gat	gaa	gtg	atc	ggt	gag	agt
88	Pro	Asp	Glu	Val	Ile	Gly	Glu	Ser
89								
91	cag	aaa	agt	cag	aaa	aga	ccc	ttc
92	Gln	Lys	Ser	Gln	Lys	Arg	Pro	Phe
93	140							
95	aag	cac	tgg	aag	cca	gct	gag	ccc
96	Lys	His	Trp	Lys	Pro	Ala	Glu	Pro
97								
99	cta	gtg	gga	cca	gtg	agc	gac	tgc
100	Leu	Val	Gly	Pro	Val	Ser	Asp	Cys
101								
103	cct	gcg	ctg	ttc	aac	cag	gag	cca
104	Pro	Ala	Leu	Phe	Asn	Gln	Glu	Pro
105								
107	aaa	acc	gac	cag	att	ccc	atg	cct
108	Lys	Thr	Asp	Gln	Ile	Pro	Met	Pro
109								
111	ctg	aat	ctc	cct	gag	gga	ccc	atc
112	Leu	Asn	Leu	Pro	Glu	Gly	Pro	Ile
113	220							
115	ctg	ccc	cat	ggg	ctc	tgg	caa	atc
116	Leu	Pro	His	Gly	Leu	Trp	Gln	Ile
117								
119	agt	ata	ttc	atc	tac	cat	ggt	gag
120	Ser	Ile	Phe	Ile	Tyr	His	Gly	Glu
121								
123	cct	ccc	agt	gga	ttc	act	gtc	cac
124	Pro	Pro	Ser	Gly	Phe	Thr	Val	His
125								
127	cca	ggc	tcc	acc	agc	ccc	ttc	gct
128	Pro	Gly	Ser	Thr	Ser	Pro	Phe	Ala
129								
131	atg	cct	gaa	cct	gcc	ctg	acc	tcc
132	Met	Pro	Glu	Pro	Ala	Leu	Thr	Ser
133	300							
135	acg	tcc	ccc	acc	caa	tgc	ccg	gca
136	Thr	Ser	Pro	Thr	Gln	Cys	Pro	Ala
137								

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139	cca	aaa	tgg	cct	gag	ccg	gtg	gag	cag	ttc	tac	cgc	tca	ctg	cag	gac	1179
140	Pro	Lys	Trp	Pro	Glu	Pro	Val	Glu	Gln	Phe	Tyr	Arg	Ser	Leu	Gln	Asp	
141				335				340						345			
143	acg	tat	ggt	gcc	gag	ccc	gca	ggc	ccg	gat	ggc	atc	cta	gtg	gag	gtg	1227
144	Thr	Tyr	Gly	Ala	Glu	Pro	Ala	Gly	Pro	Asp	Gly	Ile	Leu	Val	Glu	Val	
145			350					355					360				
147	gat	ctg	gtg	cag	gcc	agg	ctg	gag	agg	agc	agc	agc	aag	agc	ctg	gag	1275
148	Asp	Leu	Val	Gln	Ala	Arg	Leu	Glu	Arg	Ser	Ser	Ser	Lys	Ser	Leu	Glu	
149			365					370					375				
151	cgg	gaa	ctg	gcc	acc	ccg	gac	tggt	gca	gaa	cgg	cag	ctg	gcc	caa	gga	1323
152	Arg	Glu	Leu	Ala	Thr	Pro	Asp	Trp	Ala	Glu	Arg	Gln	Leu	Ala	Gln	Gly	
153	380							385					390				
155	ggc	ctg	gct	gag	gtg	ctg	ttg	gct	gcc	aag	gag	cac	cgg	cgg	ccg	cgt	1371
156	Gly	Leu	Ala	Glu	Val	Leu	Leu	Ala	Ala	Lys	Glu	His	Arg	Arg	Pro	Arg	
157				400								405					
159	gag	aca	cga	gtg	att	gct	gtg	ctg	ggc	aaa	gct	ggt	cag	ggc	aag	agc	1419
160	Glu	Thr	Arg	Val	Ile	Ala	Val	Leu	Gly	Lys	Ala	Gly	Gln	Gly	Lys	Ser	
161				415								420					
163	tat	tggt	gct	ggg	gca	gtg	agc	cgg	gcc	tggt	gct	tgt	ggc	cgg	ctt	ccc	1467
164	Tyr	Trp	Ala	Gly	Ala	Val	Ser	Arg	Ala	Trp	Ala	Cys	Gly	Arg	Leu	Pro	
165				430				435					440				
167	cag	tac	gac	ttt	gtc	ttc	tct	gtc	ccc	tgc	cat	tgc	ttg	aac	cgt	ccg	1515
168	Gln	Tyr	Asp	Phe	Val	Phe	Ser	Val	Pro	Cys	His	Cys	Leu	Asn	Arg	Pro	
169				445				450					455				
171	ggg	gat	gcc	tat	ggc	ctg	cag	gat	ctg	ctc	ttc	tcc	ctg	ggc	cca	cag	1563
172	Gly	Asp	Ala	Tyr	Gly	Leu	Gln	Asp	Leu	Leu	Phe	Ser	Leu	Gly	Pro	Gln	
173	460							465					470				
175	cca	ctc	gtg	gcg	gcc	gat	gag	ggt	ttc	agc	cac	atc	ttg	aag	aga	cct	1611
176	Pro	Leu	Val	Ala	Ala	Asp	Glu	Val	Phe	Ser	His	Ile	Leu	Lys	Arg	Pro	
177				480									485				
179	gac	cgc	ggt	ctg	ctc	atc	cta	gac	gcc	ttc	gag	gag	ctg	gaa	gcg	caa	1659
180	Asp	Arg	Val	Leu	Leu	Ile	Leu	Asp	Ala	Phe	Glu	Glu	Leu	Glu	Ala	Gln	
181				495					500					505			
183	gat	ggc	ttc	ctg	cac	agc	acg	tgc	gga	ccg	gca	ccg	gcg	gag	ccc	tgc	1707
184	Asp	Gly	Phe	Leu	His	Ser	Thr	Cys	Gly	Pro	Ala	Pro	Ala	Glu	Pro	Cys	
185				510									520				
187	tcc	ctc	cgg	ggg	ctg	ctg	gcc	ggc	ctt	ttc	cag	aag	aag	ctg	ctc	cga	1755
188	Ser	Leu	Arg	Gly	Leu	Leu	Ala	Gly	Leu	Phe	Gln	Lys	Lys	Leu	Leu	Arg	
189				525				530					535				
191	ggt	tgc	acc	ctc	ctc	ctc	aca	gcc	ccg	ccc	cgg	ggc	cgc	ctg	gtc	cag	1803
192	Gly	Cys	Thr	Leu	Leu	Leu	Thr	Ala	Arg	Pro	Arg	Gly	Arg	Leu	Val	Gln	
193	540							545					550				
195	agc	ctg	agc	aag	gcc	gac	gcc	cta	ttt	gag	ctg	tcc	ggc	ttc	tcc	atg	1851
196	Ser	Leu	Ser	Lys	Ala	Asp	Ala	Leu	Phe	Glu	Leu	Ser	Gly	Phe	Ser	Met	
197				560									565				
199	gag	cag	gcc	cag	gca	tac	gtg	atg	cgc	tac	ttt	gag	agc	tca	ggg	atg	1899
200	Glu	Gln	Ala	Gln	Ala	Tyr	Val	Met	Arg	Tyr	Phe	Glu	Ser	Ser	Gly	Met	
201				575									580				
203	aca	gag	cac	caa	gac	aga	gcc	ctg	acg	ctc	ctc	cgg	gac	cgg	cca	ctt	1947

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204	Thr	Glu	His	Gln	Asp	Arg	Ala	Leu	Thr	Leu	Leu	Arg	Asp	Arg	Pro	Leu		
205																	1995	
207	ctt	ctc	agt	cac	agc	cac	agc	cct	act	ttg	tgc	cgg	gca	gtg	tgc	cag		
208	Leu	Leu	Ser	His	Ser	His	Ser	Pro	Thr	Leu	Cys	Arg	Ala	Val	Cys	Gln		
209																		
211	ctc	tca	gag	gcc	ctg	ctg	gag	ctt	ggg	gag	gac	gcc	aag	ctg	ccc	tcc		
212	Leu	Ser	Glu	Ala	Leu	Leu	Glu	Leu	Gly	Glu	Asp	Ala	Lys	Leu	Pro	Ser		
213	620																	
215	acg	ctc	acg	gga	ctc	tat	gtc	ggc	ctg	ctg	ggc	cgt	gca	gcc	ctc	gac		
216	Thr	Leu	Thr	Gly	Leu	Tyr	Val	Gly	Leu	Leu	Gly	Arg	Ala	Leu	Asp			
217																		
219	agc	ccc	ccc	ggg	gcc	ctg	gca	gag	ctg	gcc	aag	ctg	gcc	tgg	gag	ctg		
220	Ser	Pro	Pro	Gly	Ala	Leu	Ala	Glu	Leu	Ala	Lys	Leu	Ala	Trp	Glu	Leu		
221																		
223	ggc	cgc	aga	cat	caa	agt	acc	cta	cag	gag	gac	cag	ttc	cca	tcc	gca		
224	Gly	Arg	Arg	His	Gln	Ser	Thr	Leu	Gln	Glu	Asp	Gln	Phe	Pro	Ser	Ala		
225																		
227	gac	gtg	agg	acc	tgg	gcg	atg	gcc	aaa	ggc	tta	gtc	caa	cac	cca	cgg		
228	Asp	Val	Arg	Thr	Trp	Ala	Met	Ala	Lys	Gly	Leu	Val	Gln	His	Pro	Pro		
229																		
231	cgg	gcc	gca	gag	tcc	gag	ctg	gcc	ttc	ccc	agc	ttc	ctc	ctg	caa	tgc		
232	Arg	Ala	Ala	Glu	Ser	Glu	Leu	Ala	Phe	Pro	Ser	Phe	Leu	Leu	Gln	Cys		
233	700																	
235	ttc	ctg	ggg	gcc	ctg	tgg	ctg	gct	ctg	agt	ggc	gaa	atc	aag	gac	aag		
236	Phe	Leu	Gly	Ala	Leu	Trp	Leu	Ala	Leu	Ser	Gly	Glu	Ile	Lys	Asp	Lys		
237																		
239	gag	ctc	ccg	cag	tac	cta	gca	ttg	acc	cca	agg	aag	aag	agg	ccc	tat		
240	Glu	Leu	Pro	Gln	Tyr	Leu	Ala	Leu	Thr	Pro	Arg	Lys	Lys	Arg	Pro	Tyr		
241																		
243	gac	aac	tgg	ctg	gag	ggc	gtg	cca	cgc	ttt	ctg	gct	ggg	ctg	atc	ttc		
244	Asp	Asn	Trp	Leu	Glu	Gly	Val	Pro	Arg	Phe	Leu	Ala	Gly	Leu	Ile	Phe		
245																		
247	cag	cct	ccc	gcc	cgc	tgc	ctg	gga	gcc	cta	ctc	ggg	cca	tgc	gcg	gct		
248	Gln	Pro	Pro	Ala	Arg	Cys	Leu	Gly	Ala	Leu	Leu	Gly	Pro	Ser	Ala	Ala		
249																		
251	gcc	tgc	gtg	gac	agg	aag	cag	aag	gtg	ctt	gcg	agg	tac	ctg	aag	cgg		
252	Ala	Ser	Val	Asp	Arg	Lys	Gln	Lys	Val	Leu	Ala	Arg	Tyr	Leu	Lys	Arg		
253	780																	
255	ctg	cag	ccg	ggg	aca	ctg	cgg	gcg	cgg	cag	ctg	ctt	gag	ctg	ctg	cac		
256	Leu	Gln	Pro	Gly	Thr	Leu	Arg	Ala	Arg	Gln	Leu	Leu	Glu	Leu	His			
257																		
259	tgc	gcc	cac	gag	gcc	gag	gag	gct	gga	att	tgg	cag	cac	gtg	gta	cag		
260	Cys	Ala	His	Glu	Ala	Glu	Glu	Ala	Gly	Ile	Trp	Gln	His	Val	Val	Gln		
261																		
263	gag	ctc	ccc	ggc	cgc	ctc	tct	ttt	ctg	ggc	acc	cgc	ctc	acg	cct	cct		
264	Glu	Leu	Pro	Gly	Arg	Leu	Ser	Phe	Leu	Gly	Thr	Arg	Leu	Thr	Pro	Pro		
265																		
267	gat	gca	cat	gta	ctg	ggc	aag	gcc	ttg	gag	gcg	gcg	ggc	caa	gac	ttc		
268	Asp	Ala	His	Val	Leu	Gly	Lys	Ala	Leu	Glu	Ala	Ala	Gly	Gln	Asp	Phe		

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269	845	850	855	2763
271	tcc ctg gac ctc cgc agc act ggc att tgc ccc tct gga ttg ggg agc			
272	Ser Leu Asp Leu Arg Ser Thr Gly Ile Cys Pro Ser Gly Leu Gly Ser			
273	860	865	870	2811
275	ctc gtg gga ctc agc tgt gtc acc cgt ttc agg gct gcc ttg agc gac			
276	Leu Val Gly Leu Ser Cys Val Thr Arg Phe Arg Ala Ala Leu Ser Asp			
277	880	885	890	2859
279	acg gtg gcg ctg tgg gag tcc ctg cgg cag cat ggg gag acc aag cta			
280	Thr Val Ala Leu Trp Glu Ser Leu Arg Gln His Gly Glu Thr Lys Leu			
281	895	900	905	2907
283	ctt cag gca gca gag gag aag ttc acc atc gag cct ttc aaa gcc aag			
284	Leu Gln Ala Ala Glu Glu Lys Phe Thr Ile Glu Pro Phe Lys Ala Lys			
285	910	915	920	2955
287	tcc ctg aag gat gtg gaa gac ctg gga aag ctt gtg cag act cag agg			
288	Ser Leu Lys Asp Val Glu Asp Leu Gly Lys Leu Val Gln Thr Gln Arg			
289	925	930	935	3003
291	acg aga agt tcc tcg gaa gac aca gct ggg gag ctc cct gct gtt cgg			
292	Thr Arg Ser Ser Ser Glu Asp Thr Ala Gly Glu Leu Pro Ala Val Arg			
293	940	945	950	3051
295	gac cta aag aaa ctg gag ttt gcg ctg ggc cct gtc tca ggc ccc cag			
296	Asp Leu Lys Lys Leu Glu Phe Ala Leu Gly Pro Val Ser Gly Pro Gln			
297	960	965	970	3099
299	gct ttc ccc aaa ctg gtg cgg atc ctc acg gcc ttt tcc tcc ctg cag			
300	Ala Phe Pro Lys Leu Val Arg Ile Leu Thr Ala Phe Ser Ser Leu Gln			
301	975	980	985	3147
303	cat ctg gac ctg gat gcg ctg agt gag aac aag atc ggg gac gag ggt			
304	His Leu Asp Leu Asp Ala Leu Ser Glu Asn Lys Ile Gly Asp Glu Gly			
305	990	995	1000	3195
307	gtc tcg cag ctc tca gcc acc ttc ccc cag ctg aag tcc ttg gaa acc			
308	Val Ser Gln Leu Ser Ala Thr Phe Pro Gln Leu Lys Ser Leu Glu Thr			
309	1005	1010	1015	3243
311	ctt aat ctg tcc cag aac aac atc act gac ctg ggt gcc tac aaa ctc			
312	Leu Asn Leu Ser Gln Asn Asn Ile Thr Asp Leu Gly Ala Tyr Lys Leu			
313	1020	1025	1030	3291
315	gcc gag gcc ctg cct tcg etc gct gca tcc ctg ctc agg cta agc ttg			
316	Ala Leu Ala Leu Pro Ser Leu Ala Ala Ser Leu Leu Arg Leu Ser Leu			
317	1040	1045	1050	3339
319	tac aat aac tgc atc tgc gac gtg gga gcc gag agc ttg gct cgt gtg			
320	Tyr Asn Asn Cys Ile Cys Asp Val Gly Ala Glu Ser Leu Ala Arg Val			
321	1055	1060	1065	3387
323	ctt ccg gac atg gtg tcc ctc cgg gtg atg gac gtc cag tac aac aag			
324	Leu Pro Asp Met Val Ser Leu Arg Val Met Asp Val Gln Tyr Asn Lys			
325	1070	1075	1080	3435
327	ttc acg gct gcc ggg gcc cag cag etc gct gcc agc ctt cgg agg tgt			
328	Phe Thr Ala Ala Gly Ala Gln Gln Leu Ala Ala Ser Leu Arg Arg Cys			
329	1085	1090	1095	3483
331	cct cat gtg gag acg ctg gcg atg tgg acg ccc acc atc cca ttc agt			
332	Pro His Val Glu Thr Leu Ala Met Trp Thr Pro Thr Ile Pro Phe Ser			
333	1100	1105	1110	1115

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14